

Blast 2 Sequences results

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Taxonomy

Structure

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.18 [Mar-02-2008]

Matrix gap open: gap extension:
x_dropoff: expect: wordsize: Filter ☒ View option
Masking character option Masking color option
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Sequence 1: [gi|126012562|low density lipoprotein-related protein 1 \[Homo sapiens\]](#)

Length = 4544 (1 .. 4544)

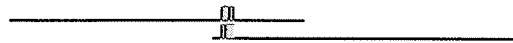
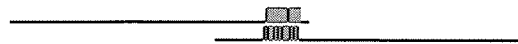
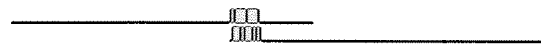
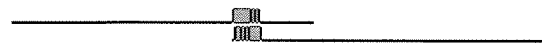
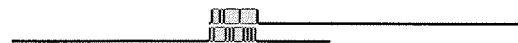
Sequence 2: [gi|126012573|low density lipoprotein-related protein 2 \[Homo sapiens\]](#)

[>gi|160332309|sp|P98164.3|LRP2_HUMAN Low-density lipoprotein receptor-related protein 2 precursor \(Megalin\) \(Glycoprotein 330\) \(gp330\)](#)

Length = 4655 (1 .. 4655)



2



Query	550	EHMIPIENLMNPR---ALDFHAETGFIYFADTTSYLIGRQKIDGTERETILKDGIHNVEG	606
		+ M+P+ NP +DF A+ I+F+D + ++I +QKIDGT RE + + + NVE	
Sbjct	731	DVMVPVSG--NPSFFVGIDFDAQDSTIFFSDMSKHMIFKQKIDGTGREILAAANRVENVES	788
Query	607	VAVDWMGDNLYWTDGPKKTISVARLEKAAQTRKTLIEGKMTHPRAIVVDPLNGWYMTD	666
		+A DW+ NLYWTD K+ISV RL A +TR+T+++ + +PR++VV P G++++TD	
Sbjct	789	LAFDWISKNLYWTD SH-YKSISVMRL--ADKTRRTVVQ-YLNNPRSVVVHPFAGYLFFTD	844
Query	667	WEEDPKDSRRGRRLERAWMDGSHRDIFVTSKTVLWPNGLSLDIPAGRLYWVDAFYDRIETI	726
		W R ++ RAW DGSH + V + T+ WENGL++D A RLYWVDA++D+IE	
Sbjct	845	W-----FRPAKIMRAWSDGSHL-LPVINTTLGWPNGLAIDWAASRLYWVDAYFDKIEHS	897
Query	727	LLNGTDRKIVYEGPELNFHAFGLCHHGNYLFWTEYRSGSVYRLERGVGGAPPTVTLLRSER	786
		+G DR+ + ++ H FGL G +LF+T++R G++ R+ + GG +T++RS	
Sbjct	898	TFDGLDRRLGHIEQMTHPFGLAIFGEHLFFTDWRLGAIIRVRKADGGE--MTVIRSGI	954
Query	787	PPIFEIRMYDAQQQVGTNKCVRN--NGGCCSLCLATPG-SRQACAEDQVLDADGVTC	842
		I ++ YD Q G+N C NG CS C P R C C L ++ +TC	
Sbjct	955	AYILHLKSVDNIQ-TGSNACNQPTHPNGDCSHFCFPVPNFRVCGCPYGMRLASNHLTC	1013
Query	843	LANPSYVPPP-QCQPGEFACANSRCIQERWKCDGDNDCLDNSDEAPALCHQHTCPSDRFK	901
		+P+ PP QC F C N RC+ + CDG +DC DNSDE +TC S F	
Sbjct	1014	EGDPTNEPPTEQCGLFSFPCKNGRCVPNYYLCDGVDDCHDNSDEQLCGTLNNTCSSSAFT	1073
Query	902	CENNRICIPNRWLCGDNDNCGNSEDESNA-TCSARTCPPNQFSCASGRICIPISWTCDLDDD	960
		C + CIP W CD NDC + DE N T + +C Q++C + +CI +W CD D+D	
Sbjct	1074	CGHGECIPAHWRCDKRND CVDGSDEHNCPHAPASCLDTQYTCDNHQCISKNWVCDTDND	1133
Query	961	CGDRSDESASCAYPTCFPLTQFTCNNGRCININWRCDNDNDCGDNSDEAGCSHSCSSTQF	1020
		CGD SDE + TC P +QF C N RCI++++ CD D DC D SDE GC +C+++QF	
Sbjct	1134	CGDGSDEKNCNSTETCQP-SQFNCPNHRCIDLSFVCDGDKDCVDGSDEVGCVLNCTASQF	1192
Query	1021	KCNSG-RCIPEHWTCGDNDNCGDYSDETHANCTNQATRPPGGCHTDEFQCRLDGLCIPLR	1079
		KC SG +CI CDG DC D SDE A C TRPPG CH+DEFQC+ DG+CIP	
Sbjct	1193	KCASGDKCIGVTNRCDGVFDCSDNSDE--AGCP--TRPPGMCHSDEFQCQEDGICIPNF	1247
Query	1080	WRCDGDTDCMDSSDEKSCEGVTHVCDPSVKFGCKDSARCISKAWVCDGDNDCEDNSDEEN	1139
		W CDG DC+ SDE + V C PS F C D+ CI +AW+CD DNDC D SDE++	
Sbjct	1248	WECDHDPDCLYGSDEHNA-CVPKTC-PSSYFHC-DNGNCIHRWLCDRDNDCGDMSDEKD	1304
Query	1140	CESLACRPPSHP---CANNTSVCLPPDKLCDGNDDCGDGSDEGELCDQCSLNNGGCSHNC	1196
		C + R PS +N V L + G + CS NGGC+H C	
Sbjct	1305	CPTQPFRCPSWQWQCLGHNICVNLVSVCDGIFDCPNGTDESPLCNGNSCSDFNNGGCTHEC	1364
Query	1197	SVAPGEGIVCSCPLGMELGPDNHTCQIQSYCAHLKCSQKCDQNKFSVKCSCYEGWVLEP	1256
		P G C CPLG L D+ TC+ C CSQ C + S +CSC G++LE	
Sbjct	1365	VQEPF-GAKCLCPLGFLLANDSKTCEDIDECIDILGSCSQHCYNMRGSFRCSCDTGYMLES	1423
Query	1257	DGESCRSLDPFKPFIIFSNRHEIRRIDLHKGDISV--LVPGLRNTIALDFHLSQSALYWT	1314
		DG +C+ ++ +++++I + +++ LV +A+DF ++W+	
Sbjct	1424	DGRTCKVTASESLLLLVASQNKIIADSVTSQVHNIYSLVENGSIYIVAVDFDSISGRIFWS	1483
Query	1315	DVVEDKIYRGKLLDNGALTSFEVVIQYGLATPEGLAVDWIAGNIYWVESNLDQIEVAKLD	1374
		D + K + NG T VV + E +A+DW+ N+YW + L+ IEV+K+D	
Sbjct	1484	DATQGKTWSA--FQNG--TDRRVVFDSSIIILTETIAIDWVGRNLYWTDYALETIEVSKID	1539
Query	1375	GTLRTTLLAGDIEHPRAIALDPR--DGILFWTDWDASLPRIEAAASMSGAGRRTVHRETGS	1432
		G+ RT L++ ++ +PR +ALDPR + +LFW+DW PRIE ASM G+ R + ++	
Sbjct	1540	GSHRTVLISKNLNTPRGLALDPRMNEHLLFWSWDGHH-PRIERASMDGSMRTVIVQDKIF	1598
Query	1433	GGWPNGLTVDYLEKRILWIDARSDAIYSARYDGS GHMEVLRGHEFLSHPFVAVTLYGGEVY	1492
		WP GLT+DY + + ++D+ D + Y+G +V+ + HP+A+TL+ VY	
Sbjct	1599	--WPCGLTIDYPNRLLYFMDSYLDYMDFCDYNHGHRRQVIASDLIIRHPYALTFLFEDSVY	1656

Query	1493	WTDWRTNTLAKANKWTGHNVTVVQRTNTQPFDLQVYHPSRQPMAPNPCEANGGQGPCSHL	1552
		WTD T + +ANKW G N +VV P + HPS+QP + NPC + CSHL	
Sbjct	1657	WTDRASTRVVRANKWHGGNQSVVMYNIQWPLGIVAVHPSKQPNSVNPACAFSR---CSHL	1712
Query	1553	CLINYN--RTVSCACPHLMKLHKDNTTCY-EFKKFLLYARQMEIRGVLDLAPYYNYIISF	1609
		CL++ SC CP L D C + + FL+ RQ I G+ L+ +	
Sbjct	1713	CLLSSQGPFPYFSCVCPGWSLSPDLLNCLRDDQPFLLITVRQHIIIFGISLNPEVKNSNDAMV	1772
Query	1610	TVPDIDNVTVLDYDAREQRVYWSVVRTQAIAKRAFINGTGVETVVSADLPN-AHGLAVDWV	1668
		+ I N +++D EQ +YW + I R +GT S + + LA+DW+	
Sbjct	1773	PIAGIQNGLDVEFDAAEQYIYWVE-NPGEIHRVKTDGTNRNRTVFASISMVGPSPMNLALDWI	1831
Query	1669	SRNLFWTSYDTNKKQINVARLDGSFKNVAVVQ-----GLEQPHGLVVHPLRGKLYWTDGD	1722
		SRNL+ T+ T ++ D ++ ++ G+ P G+ V P RGKLYW+D	
Sbjct	1832	SRNLYSTNPRTQSIEVLTLLHGDIRYRKTLIANDGTALGVGFPIGITVDPARGKLYWSDQG	1891
Query	1723	N-----ISMANMDGSNRTLLFSGQKGPVG-LAIDFPESKLYWISSGNHTINRCNLDGS	1774
		I+ ANMDG++ LF+G + + +D E KLYW +G I R N+DG+	
Sbjct	1892	TDSGVPAKIASANMDGTSVKTLFTGNLEHLECVTLDIEEQKLYWAVTGRGVIERGNVDGT	1951
Query	1775	GLEVIDAMRSQLGKATALAIMGDKLWWADQVSEKMGTCADGSGSVVLRNSTTLVMHMK	1834
		++ QL +A+ L++ D+ E + KA G+ +VLR++ + ++	
Sbjct	1952	DRMILV--HQLSHPWGIADVHDSFLYYTDEQYEVIERVDKATGANKIVLRDNVPLRGLQ	2008
Query	1835	VYDESIQLDHKGTNPSCSVNNGDCSQLCLPTSETTRSCMCTAGYSLRSGQQACEGVGSFLL	1894
		VY + +N CS N C Q+CLP SC C G+ L ++C SF++	
Sbjct	2009	VYHRRNAE--SSNGCSNMNACQQICLPVPGGLFSCACATGFKLNPDNRSCSPYNSFIV	2066
Query	1895	YSVHEGIRGIPLDPNDKSDALVPVSGTSL-AVGIDFHAENDTIYWVDMGLSTIS-----R	1948
		S+ IRG L+ +D S+ +VPV+G A+ +D + IYW D S S R	
Sbjct	2067	VSMLSAIRGFSLELSDHSETMVPVAGQGRNALHVDVDVSSGFIYWCDFSVSSVADNAIRR	2126
Query	1949	AKRDQTWREDVVTNGIGR--VEGIAVDWIAGNIYWTQDQFD--VIEVARLNGSFRYVVIS	2004
		K D + ++VT+GIG V GIAVDW+AGN+Y+T+ +IEV R+N ++R V++	
Sbjct	2127	IKPDGSSLMNIVTHGIGENGVRGIAVDWVAGNLYFTNAFVSETLIEVLRINTTYRRVLLK	2186
Query	2005	QGLDKPRAITVHPEKGYLFWTEWGQYPRIERSRLDGTERVVLVNVSISWPNGISVDYQDG	2064
		+D PR I V P+ YLFW ++GQ P+IERS LD T R VLV+ I P G++VD DG	
Sbjct	2187	VTVDMPRHIVDPKNRYLFWADYGQRPKIERSFLDCTNRTVLVSEGIPTPRGLAVDRSDG	2246
Query	2065	KLYWCDARTDKIERIDLETGENREVV-LSSNNMDMFSVSVFEDFIYWSDRTHANGSIKRG	2123
		+YW D D I RI + GEN EV+ S + ++VFE+ I W DR	
Sbjct	2247	YVYWVDDSLDIARIRIN-GENSEVIRYGSRYPTPYGITVFENSIWVDRNLKKIFQASK	2305
Query	2124	SKDNATDSVPLRTGIGVQLKDIKFVNRDRQK-----GTNVCVAVANGGCQQLCL-YRGRG	2176
		+N +R I L+D+ +F++ Q N C NGGC LC G	
Sbjct	2306	EPENTEPPTVIRDNIN-WLRDVTIFDKQVQPRSPAENVNNPCLENNGGCCHLCFALPGLH	2364
Query	2177	QRACACAHGMLAEDGASCR-EYAGYLLYSERTILKSIHLSDERNLNAPVQPFEDPEHMK	2235
		C CA G L DG +C +L+++ L+S+HL E + PF+ +	
Sbjct	2365	TPKCDCAFGLTQSDGKNCAISTENFLIFALSNSLRSLHLDPENHS----PPFQTINVERT	2420
Query	2236	VIALAFDYRAGTSPGTPNRIFFSDIHFGNIQQIN----DDGSRRITIVEN-VGSVEGLAY	2290
		V++L +D +RI+F+ + QI+ G T++ + +G+ +G+A+	
Sbjct	2421	VMSLDYD-----SVSDRIYFTQNLASGVGQISYATLSSGIHTPTVIASGIGTADGIAF	2473
Query	2291	HRGWDTLYWTSYTTSTITRHTVDQTRPGAFAFERETVITMSGDDHPRAFLVDECQNLMFWTN	2350
		D + Y + + + G+ TVI PRA VLD CQ ++W +	
Sbjct	2474	----DWITRRIYSDYLNQMINSMAEDGS--NRTVIARV--PKPRAIVLDPCQGYLYWAD	2525
Query	2351	WNEQHPSIMRAALSGANVLTLEKDIRTPNGLAIDHRAEKLYFSDATLDKIERCEYDGS	2410
		W + H I RA L G + ++ + P+GL +D+ + LY+ DA+L +IER G	
Sbjct	2526	W-DTHAKIERATLGGNFRVPIVNSSLVMPGSLTLDYEEDLLYWVDASLQRIERSTLTGVD	2584

Query	2411	RYVILKSEPVHFPGLAVYGEHIFWTDWVRRVQRANKHVGSNMKLLRVDIPQQPMGI-IA	2469
		R VI+ + VH FGL +YG++I+WTD + + RANK+ GS + ++ QP GI	
Sbjct	2585	REVIVNAA-VHAFGLTLYGQYIYWTDLYTQRIYRANKYDGSQIAMTTNLLSQPRGINTV	2643
Query	2470	VANDTNSCELSPCRINNGGCQDLCLLTHQGHVNCSC--RGGRILQDDLT-CRAVNSSCRA	2526
		V N C +PC NGGC +C G C C G L ++ C N	
Sbjct	2644	VKNQKQQCN-NPCEQFNGGCSHICAPGPNG-AECQCPHEGNWYLANNRKHCIVDNGERCG	2701
Query	2527	QDEFECANGECINFSLTCDGVPHCKDKSDEKPSYCNSRRCKKTFRQCSNGRCVSNMLWCN	2586
		F C+NG CI+ CD C D SDE S C C T C+NGRCV C+	
Sbjct	2702	ASSFTCSNGRCISEEWKCDNDNDCGDGSDMESVCALHTCSPTAFTCANGRCVQYSYRCD	2761
Query	2587	GADDCGDGSDSEIPCNTACGVG-EFRCRDGTCIGNSSRCNQFVDCED--ASDEMNC SATD	2643
		+DCGDGSDSE C C EF C + CI CN +C D SDE NC	
Sbjct	2762	YYNDCGDGSDSEAGCLFRDCNATTEFMCNNRRCIPREFICNGVDNCHDNNTSDEKNCPDRT	2821
Query	2644	CSSYFRLGVKGVLFQPCERTSLCYAPSWVCDGANDCGDYSDERDCPGVKRPRCPLNYFAC	2703
		C S + C +++C ++CDG NDCGD SDE C + F C	
Sbjct	2822	CQSGYT-----KCHNSNICIPRVYLCGDNDNCGDNDENPTYCTTHT-CSSSEFQC	2871
Query	2704	PSGRCIPMSWTCDKEDDCEHGEDET----HCNKFCSEAQFECQNHRCISKQWLCDGSDDC	2759
		SGRCIP W CD+E DC DE H + C +F+C RCI +W+CDG +DC	
Sbjct	2872	ASGRCIPQHWYCDQETDCFDASDEPASCCHSERTCLADEFKCDGGRCIPSEWICDGDNDNDC	2931
Query	2760	GDGSDAAH--CEGKTCGPSSFSC---PGTHVCVPERWLCGDGDKCADGADESIAAGCL	2813
		GD SDE C+ + C S F C P C+P+ W+CDGD DC DG DE+ C	
Sbjct	2932	GDMSDEDKRHCQCNQNCSDSEFLCVNDRPPDRRCIPQSWVCDGDVDCTDGYDEN--QNCT	2989
Query	2814	YNSTCDDREFMCQNRQCIPKHFVCDHDRDCADGSDSEPECEYPTCGPSEFRCANGRCLSS	2873
		TC + EF C CIPK F CD DC D SDE C Y TC ++F C NGRC+S	
Sbjct	2990	-RRTCSENEFTCGYGLCIPKIFRCDRHNDNCGDYSDERG-CLYQTCQQNQFTCQNGRCIS-	3046
Query	2874	RQWECGDGENDCHDQSDEAPKNPHCTSQEHKCNASSQFLCSSGRCVAEALLCNGQDDCGDS	2933
		+ + CD +NDC D SDE C + E C +F C +GRC+ LCN DDC D+	
Sbjct	3047	KTFVCEDEDNDCGDGSDDELMHL--CHTPEPTC-PPHEFKCDNGRCIEMMKLCNHLDDCLDN	3103
Query	2934	SDERGCHINECLSRKLSGCSQDCEDLKIGFKRCRCPGFRLKDDGRTCADVDECSTT-FPC	2992
		SDE+GC INEC +SGC +C D F C CRPG++L D RTC D+DEC+ F C	
Sbjct	3104	SDEKGCGINECHDPSISGCDHNCTD'TLTSFYCSCRPGYKLMSDKRTCVDIDECTEMPFCV	3163
Query	2993	SQRCINTHGSYKCLCVEGYAPRGDPHSCKAVTDEEPFLIFANRYYLRLKLNLDGSNYTLL	3052
		SQ+C N GSY C C GY R D +C+ ++ EP+LIF+NRYYLRL +DG Y+L+	
Sbjct	3164	SQKCEENVIGSYICKAPGYL-REPDGKTCRQNSNIEPYLIFSNRYYLRNLTIDGYFYSLI	3222
Query	3053	KQGLNNAVALDFDYREQMIYWTDVTTQGSIMRRMHLNGSNVQVLHRTGLSNPDGLAVDWV	3112
		+GL+N VALDFD E+ +YW D TQ +I RM LN +N + + L + LAVDWV	
Sbjct	3223	LEGLDNVVALDFDRVEKRLYWID--TQRQVIERMFLNKTNKETIINHRLPAAESLAVDWV	3280
Query	3113	GGNLYWCDKGRDTIEVSKLNGAYRTVLVSSGLR-----EPRALVVDVQNGYLYWTDW	3164
		LYW D D + VS LNG +R +L + PR L + Q GYLYW DW	
Sbjct	3281	SRKLYWLDARLDGLFVSDLNGGHRMLAQHCVDANNTFCFDNPRGLALHPQYGYLYWADW	3340
Query	3165	GDHSLIGRIGMDGSSRSVIVDTKITWPNGLTLDYVTERIYWADAREDYIEFASLDGSNRH	3224
		G + IGR+GMDG+++SVI+ TK+ WPNG+T+DY + +YWADA YIE++ L+G +RH	
Sbjct	3341	GHRAYIGRVGMDGTNKSVIISTKLEWPNGITIDYTNDLLYWADAHLGYIEYSDLEGHHRH	3400
Query	3225	VVLSQDIPHIFALTLFEDYVYWTDWETKSINRAHKTGTGNTKLLISTLHRPMDLHV FHAL	3284
		V +PH FA+T+FED +YWTDW T+++ + +K G+N+ L++T HRP D+HV+H	
Sbjct	3401	TVYDGALPHPFATIFEDTIYWTDWNTRTVEKGNGKYDGSNRQTLVNTTHRPFDIHVYHPY	3460
Query	3285	RQPDVPNHPCKVNNGGCSNLCLLSPGG-GHKACPTNF-YLGS DGRT-CVSNCTASQFVC	3341
		RQP V N PC NNGGCS+LCL+ PGG G C CP +F L G T C+ C+++QF+C	
Sbjct	3461	RQPIVSN-PCGTNNGGCSHLCLIKPGKGFTCECPDDFRTLQLSGSTYCMPCMSSTQFLC	3519

Query	3342	-KNDKCIPFWWKCDTEDDCGDHSDEPPDCPEFKCRPGQFQCSTGICTNPAFICDGDNDQC N+KCIP WWKCD + DC D SDE CP+ CR GQFQCS G CT+P +C+ +C	3400
Sbjct	3520	ANNEKCIPIWWKCDGQKDCSDGSDELALCPQRFRCRLGQFQCSDGNCTSPQTLCAHQNCP	3579
Query	3401	DNSDEAN--CDIHVCLPSQFKCTNTNRCIPGIFRCNGQDNCGDG--EDERDCPEVTCAPN D SDE C+ H C ++++C N RCIP ++C+ ++C D ED C TC P	3456
Sbjct	3580	DGSEDEDLLCENHHCDNSNEWQCAN-KRCIPESWQCDTFNDCEDNSDEDSSHCASTRCPG	3638
Query	3457	QFQCSITKRCIPRVVWCDRDNDICVDGSDEP----ANCTQMTGCVDEFRCCKDSGRICIPARW QF+C+ RCIP+ W CD DNDC D SDEP + + EF CK + RCIP +W	3512
Sbjct	3639	QFRCA-NGRCIPQAWKCDVDNDCGDHSDEPIIECMSSAHLCDNFTEFSCKTNYRCIP-KW	3696
Query	3513	KCDGEDDCGDGSDEPKKECDERTCEPY-QFRCKNNRCVPGRWQCDYDNDCGDNSDEESCT + ++ C+ERTC P FRCKN+ C+P RWQCD NDCGDNSDEE+C	3571
Sbjct	3697	-AVCNGVDDCRDNSDEQGCEERTCHPVGDFRCKNHHCIPLRWQCDGQNDCGDNSDEENCA	3755
Query	3572	PRPCSESEFSCANGRCIAGRWKCDGDHDCADGSDEKDCCTPR-CDMDQFQCKSGHCIPLRW PR C+ESEF C N +CI RW CD +DC D SDE+DC R C + FQC SGHC+	3630
Sbjct	3756	PRECTESEFRVCNQQCIPSRWICDHYNDCGDNSEDERDCMRTCHPEYFQCTSGHCVHSEL	3815
Query	3631	RCDADADCMDGSDEEACGTGV---RTCPLDEFQCNNTLCKPLAWKCDGEDDCGDNSDENP +CD ADC+D SDE C T C F+C N +C P WKCDG+DDCGD SDE	3687
Sbjct	3816	KCDGSADCLDASDEADCPTRFPDGAYCQATMFECKNHVCIPPYWKCDGDDDCGDGSDEEL	3875
Query	3688	EECARFVCPNRPFRCKNDRVCLWIGRQCDGTNCGDGTDEEDCEPPTAHTTHCKDKKEF C C FRC N+R C++ C+G D+CGDGTDE + C + E+	3747
Sbjct	3876	HLCLDVPCNSPNRFRCDNNR-CIYSHEVCNGVDDCGDGTDETEEHCRKPTPKPCTE-YEY	3933
Query	3748	LCRNQRCLSSSLRCNMFDDCGDGSDEEDCSIDPKLTSCATNASICGDEARCVRTEKAAAY- C N C+ C+ DDCGD SDE C+ K +CA N IC E C + + +	3806
Sbjct	3934	KCGNGHCIPHDNVCDADDCGDWSDELGCN-KGKERTCAEN--IC--EQNCTQLNEGGFI	3988
Query	3807	CACRSGFHT-VPGQPGCQDINECLRFGTCSQLCNNTKGGHLCSCARNFM----KTHNTCK C+C +GF T V + C DINEC +FGTC Q C NTKG + C CA F + C	3861
Sbjct	3989	CSCTAGFETNVFDRTSCLDINECEQFGTCQHCNRTKGSYECVCADGFTSMSDRPGKRCA	4048
Query	3862	AEGSEYQVLYIADDNEIRSL-FPGHPSAYEQAFQGDSESVRIDAMDVHVKAGRVYWTNWH AEGS +L + D+ IR S Y Q + ++V D + VY+T	3920
Sbjct	4049	AEGSS-PLLLLPDNVRIRKYNLSSERFSEYLQDEEYIQAVDYDWDPKDIGLSVYYTVRG	4107
Query	3921	TGTISYRSLPPAAPPTTSNRHRRQIDRGVTHLNISGLKMPRGIAIDWVAGNVYWTDSGRD G+ + ++ A P + + L + + P GIA+DWV ++YW+D	3980
Sbjct	4108	EGS-RFGAIKRAYIPNFESGRNNLVQE--VDLKLKYVMQPDGIAVDWVGRHIYWSDVKNK	4164
Query	3981	VIEVAQMKGENRKTLLISGMIDEPHAIVVDPLRGTMYSWDWGNHPKIEAAMDGTLRETLV IEVA++ G RK LIS +D+P AI V+P G M+W+DWG PKIE+A M+G R LV	4040
Sbjct	4165	RIEVAKLDGRYRKWLSTDLQPAIAVNPKLGLMFWTDWGKEPKIESAWMNGEDRNILV	4224
Query	4041	QDNIQWPTGLAVDY-HNERLYWADAKLSVIGSIRLNGTDPIVAADSKRGLSHPFSDVFE +++ WPTGL++DY +N+R+YW+D K VI +I+ +GTD V A + +P+S+D+FE	4099
Sbjct	4225	FEDLGWPTGLSIDYLNNDRIYWSDFKEDVIETIKYDGTDRRVIA---KEAMNPYSLDIFE	4281
Query	4100	DYIYGVTYINNRFVKIHKFGHSPLVNLTGGLSHASDVVLYHQHK-QPEVTNPCKRKKCEW D +Y ++ V+K +KFG + V ++HQ + V N C ++ C	4158
Sbjct	4282	DQLYWISKEKGEVWVKQNKFGQKKEKTLVNPWLTVQVRIHFHQLRYNKSVPNLC-KQICSH	4340
Query	4159	LCLLSPSGPVCTCPNGKRLDNGTCVPVPSPPTPPDAPRPGTCNLQCFNGGSCFLNARRQP LCLL P G C CP G G+ + P P +C +GG+C+ + P	4218
Sbjct	4341	LCLLRPGGYSCACPGSSFIEGSTTECDAAIELPINLPP---PCRCMHGGNCYFDETDLP	4397
Query	4219	KCRCQPRYTGDKCEL 4233 KC+C YTG CE+	
Sbjct	4398	KCKCPSGYTGKYCEM 4412	



Score = 595 bits (1535), Expect = 4e-167

Identities = 372/1068 (34%), Positives = 536/1068 (50%), Gaps = 88/1068 (8%)

Query	840	VTCLANPSYVPPPPQCQPGFACANSRCIQERWKCDGDNDCLDNSDEAPALCHQHTCPSDR	899
		V CLA S +C F C + CI W+CDG DC D++DE C TC	
Sbjct	17	VACLAPAS---GQECDSAHRFCGSGHCIPADWRCDGTDKCSDDADEIG--CAVVTCQQGY	71
Query	900	FKCENN-RCIPNRWLCGDNDNCGNSEDESNATCSARTCPPNQFSCASGRICIPISWTCDL	958
		FKC++ +CIPN W+CD D DC + DE CS TC +Q +C++G+CIP + CD	
Sbjct	72	FKCQSEGCIPNSWVCDQDQDCDDGSDERQ-DCSQSTCSSHQITCSNGQIPSEYRCDHV	130
Query	959	DDCGDRSDESASCAYPTCFPLTQFTCNNGRCININWRCDNDNDCGDNNSDEAGCSHSCSST	1018
		DC D +DE+ C YPTC Q TC+NG C N + +CD DC D+SDE C+ C	
Sbjct	131	RDCPDGADEN-DCQYPTC---EQLTCDNGACYNTSQKCDWKVDCRDSSDEINCTEICLHN	186
Query	1019	QFKCNSGRCIPEHWTCGDNDNCGDYSDETHANCTNQATRPFGGCHTDEFQCRLDGLCIPL	1078
		+F C +G CIP + CD DNDC D SDE N C +F C G CI	
Sbjct	187	EFSCGNCECIPRAYVCDHDNDCQDGSDEHACNYPT-----CGGYQFTCP-SGRCIYQ	237
Query	1079	RWRCDGDTDCMDSSDEKSCEG---VTHVCDPSVKFGCKDSARCISKAWVCDGDNDCEDNS	1135
		W CDG+ DC D+ DE CE H C P ++ C +S RCIS VCDG	
Sbjct	238	NWVCDGEDDCKDNGDEDGCESGPHDVHKCSPR-EWSCPESGRCSISYKVC DG-----	288
Query	1136	DEENCESLACRPPSHPCANNTSVCLPPDKLCDGNDDCGDGSDEGELCDQCSLNNGGCSHN	1195
		L C P NNTS + CS N C +	
Sbjct	289	-----ILDC--PGREDENNTST-----GKYCSMTLCSALN--CQYQ	320
Query	1196	CSVAPGEGIVCSCPLGMELG-PDNHTCQIQSYCAKHLKCSQKCDQNKFSVKCSCYEGWVL	1254
		C P G C CP G + D+ TC C C QKC+ C C EG++L	
Sbjct	321	CHETPYGG-ACFCPPGYIINHNDRTCEVFDDCQIWGICDQKCESRPGRHLCHCEEYIL	379
Query	1255	EPDGESCRSLDPF-KPFIIFS NRHEIRRIDLHKGDYSVLVPLRNTIALD--FHLSQSAL	1311
		E G+ C++ D F + IIFSN ++ D+H + +LV +A+ FH +	
Sbjct	380	E-RGQYCKANDSFGEASIIIFSNGRDLIGDIHGRSFRILVESQNRGVAVGVAFHYHLQRV	438
Query	1312	YWTDVVEDKIIYRGKLLDNGALTSFEVVIQYGLATPEGLAVDWIAGNIYWVESNLDQIEVA	1371
		+WTD V++K++ + NG + + V+ + TPE LAVDW+ IY VE+ +++I++	
Sbjct	439	FWTDTVQNKVFSVDI--NG--LNIQEVLVNSVETPENLAVDWVNNKIYLVETKVNRI DMV	494
Query	1372	KLDGTLRTTLLAGDIEHPRAIALDPRDGILFWTDWD--ASLPRIEAASMSGAGRRTVHRE	1429
		LDG+ R TL+ ++ HPR IA+DP G LF++DW+ + P++E A M G+ R+ + +	
Sbjct	495	NLDGSYRVTLITENLGHPRGIAVDPTVGYLFFSDWESLSGEPKLERAFMDGSNRKDLVKT	554
Query	1430	TGSGGWPNGLTVDYLEKRILWIDARSDAIYSARYDGS GHMEVLRGHEFLSHPFVAVTLYGG	1489
		GWP G+T+D + KR+ W+D+R D I + YDG V+ G + HPF V+L+ G	
Sbjct	555	--KLGWPAGVTLDMISKRVYVWDSRFDYIETVYTDGIQRKTVVHGGSLIPHPFGVSLFEG	612
Query	1490	EVYWTDWRTNTLAKANKWTGHNVTVVQRTNTQPFDLQVYHPSRQPMAPNPCEANGGQGPC	1549
		+V++TDW + KANK+T N V + + +P+ + VYH RQP A NPC+ N G C	
Sbjct	613	QVFFTDWTKMAVLKANKFTETNPQVYQASLRPYGVTVYHSLRQPYATNPCKDN--NGGC	670
Query	1550	SHLCLINYNRT-----VSCACPHLMKLHKDNTTCYEFKKFLLYARQMEIRGVDLDAPYYN	1604
		+C++++ C C +L D C + FL+++ Q+ IRG+	
Sbjct	671	EQVCVLSHRTDNDGLGRCKCTFGFQLDTERHCAVQNFLIFSSQVAIRGIPFTLSTQE	730
Query	1605	YIISFTVPDIDNVTVLDDYDAREQRVYWSDVRTQAIKRAFINGTGVETTVVSADLPNAHGLA	1664
		++ + +D+DA++ +++SD+ I + I+GTG E + + + N LA	

Sbjct 731 DVMVPVSGNPSFFVVGIDFDAQDSTIFFSDMSKHMIFKQKIDGTGREILAAANRVENVESLA 790

Query 1665 VDWVSRNLFWTSYDTNKKQINVARLDGSFKNAVVGLEQPHGLVVHPLRGKLYWTD---G 1721
DW+S+NL+WT D++ K I+V RL + VVQ L P +VVHP G L++TD

Sbjct 791 FDWISKNLWT--DSHYKSISVMRLADKTRRTVVQYLLNPRSVMVHPFAGYLFFTDWFRP 848

Query 1722 DNISMANMDGSNRTLLFSGQKG-PVGLAIDFPESKLYWISSGNHTINRCNLDGSGLEVID 1780
I A DGS+ + + G P GLAID+ S+LYW+ + I DG +

Sbjct 849 AKIMRAWSDGSHLLPVINTTLGWPNGLAIDWAASRLYWVDAYFDKIEHSTFDGLDRRLG 908

Query 1781 AMRSQLGKATALAIMGDKLWWADQVSEKMGTCISKADGSGSVVLRNSTTLVMHMKVYDESI 1840
+ Q+ LAI G+ L++ D + KADG V+R+ ++H+K YD +I

Sbjct 909 HI-EQMTHPFGLAIFGEHLFFTDWRLGAIIRVRKADGGEMTVIRSGIAYILHLKSYDVNI 967

Query 1841 QLDHKGTPNPSVNNGDCSQLCLPTSETTRSCMCTAGYSLRSGQQACEG 1888
Q N + NGDCS C P R C C G L S CEG

Sbjct 968 QTGSNACNQPTHPNGDCSHFCFPVPNFQVCGCPYGMRLASNHLTCEG 1015



Score = 428 bits (1100), Expect = 1e-116

Identities = 261/716 (36%), Positives = 367/716 (51%), Gaps = 56/716 (7%)

Query 2640 SATDC-SSYFRLGVKGVLFQPCERTSLCYAPSWVCDGANDCGDYSDERDCPGVKRPRCPL 2698
S +C S++FR G + C W CDG DC D +DE C V C

Sbjct 24 SGQECDSAHFRCG-----SGHCIPADWRCDGTDKDCSDDADEIGCAVVT---CQQ 69

Query 2699 NYFACPS-GRCIPMSWTCDEKDDCEHGEDETH-CNKF-CSEAQFECQNHRCISKQWLCDG 2755
YF C S G+CIP SW CD++ DC+ G DE C++ CS Q C N +CI ++ CD

Sbjct 70 GYFKCQSEGQCIPNSWVCDQDQDCDDGSDERQDCSQSTCSSHQITCSNGQCIPSEYRCDH 129

Query 2756 SDDCGDGSDEAAHCEGKTCGPSSFSCPGTHVCVPERWLCGDGDKCADGADESIAAGCLYN 2815
DC DG+DE C+ TC +C + + + CL+N

Sbjct 130 VRDCPDGADEN-DCQYPTC--EQLTCDNGACYNTSQKCDWKVDCRDSSDEINCTEICLHN 186

Query 2816 STCDDREFMCQNRQCIPKHFVCDHDCADGSDESPECEYPTCGPSEFRCANGRLSSRQ 2875
EF C N +CIP+ +VCDHD DC DGSDE C YPTCG +F C +GRC+ +

Sbjct 187 -----EFSCNGECIPRAYVCDHDNDQDGSDEHA-CNYPTCGGYQFTCPSGRCIY-QN 238

Query 2876 WECGDGENDCHDQSD--APKNPHCTSQEHKCNASSQFLCSSGRCVAEALLCNGQDDCGDS 2933
W CDGE+DC D DE PH HKC+ SGRC++ +C+G DC

Sbjct 239 WVCDGEDDCKDNGDEDCESGPH---DVHKCSPREWSCPESGRCISIIYKVC DGILDCPGR 295

Query 2934 SDERGCHINECLSRKLSG---CSQDCEDLKIGFKRCRPGFRLK-DDGRTCADVDECSTT 2989
DE + S L C C + G C C PG+ + +D RTC + D+C

Sbjct 296 EDENNTSTGKYCSMTLCSALNCQYQCHETPYGGACFCPPGYIINHNDSTRTCVEFDDCQIW 355

Query 2990 FPSCQRCINTHGSYKCLCVEGYAPRGDPHSCKAVTD-EEPFLIFANRYYLRLKNLDGSN 3048
C Q+C + G + C C EGY G CKA E +IF+N L ++ G +

Sbjct 356 GICDQKCESRPGRHLCHCEEYILERGQ--YCKANDSFGEASIIIFSNGRDLLIGDIHGRS 413

Query 3049 YTLLKQGLNNAVALD--FDYREQMIYWTDVTTQGSIMRRMHLNGSNVQVLHRTGLSNPDG 3106
+ +L + N VA+ F Y Q ++WTD T + + + +NG N+Q + + P+

Sbjct 414 FRILVESQNRGVAVGVAFHYHLQRVFWTD--TVQNKFVSVDINGLNIQEVNLVSVETPEN 471

Query 3107 LAVDWVGGNLYWCDKGRDTIEVSKLNGAYRTVLVSSGLREPRALVVDVQNGYLYWTDWGD 3166
LAVDWV +Y + + I++ L+G+YR L++ L PR + VD GYL+++DW

Sbjct 472 LAVDWVNNKIYLVETKVNRIIDMVNLDGSYRVTLITENLGHPRGIAVDPTVGYLFFSDWES 531

Query 3167 HS---LIGRIGMDGSSRSVIVDTKITWPNGLTLDYVTERIYWADAREDYIEFASLDGSNR 3223


```
S      + R  MDGS+R  +V TK+ WP G+TLD +++R+YW D+R DYIE  + DG  R
Sbjct  532  LSGEPKLERAFMDGSNRKDLVKTKLGWPAGVTLDMISKRVYVWDSRFDYIETVTVYDGIQR  591

Query  3224  HVVL--SQDIPHIFALTLFEDYVYWTDWETKSINRAHKTGTGNTKLLISTLHRPMDLHVF  3281
          V+      IPH F ++LFE  V++TDW  ++ +A+K T TN  +      RP  + V+
Sbjct  592  KTVVHGGSLIPHFPFVSLFEGQVFFTDWTKMAVLKANKFTETNPQVYYQASLRPYGVTVY  651

Query  3282  HALRQPDVPNHPCKVNNGGCSNLCLLS-----PGGGHKCACPTNFYLGSDGRTCVS  3332
          H+LRQP  N PCK NNGGC +C+LS      G G +C C  F L +D R C++
Sbjct  652  HSLRQPYATN-PCKDNNGGCEQVCVLSHRTDNDGLGFRCKCTFGFQLDTERHCIA  706
```



Score = 376 bits (966), Expect = 4e-101

Identities = 267/841 (31%), Positives = 407/841 (48%), Gaps = 58/841 (6%)

```
Query  24    PKTCSPKQFACRDQITCISKGWRCDCGERDCPDGSDEAPEICPQSKAQRCPNEHNCLGTE  83
          PKTC      F C D  CI + W CD + DC D SDE  CP ++ RC  + CLG
Sbjct  1268  PKTCPSSYFHC-DNGNCIHRALCDDRNDGCDMSDEKD--CP-TQPFRCPSWQWQCLGHN  1323

Query  84    LCVPM SRLCNGVQDCMDGSDEGPHCRELQGNCSRLGCHCVPTLDGPTCYCNSSFQLQA  143
          +CV +S +C+G+ DC +G+DE P C      +   GC H CV  G C C  F L
Sbjct  1324  ICVNLSVVCDFGIFDCPNGTDESPLCNGNSCSDFNNGGCTHECVQEPFGAKCLCPLGFLAN  1383

Query  144    DGKTCKDFDECSVYGTCSQLCTNTDGSFICGCVGYLLQPDNRCKAKNEPVD RPPVLLI  203
          D KTC+D DEC + G+CSQ C N  GSF C C  GY+L+ D R+CK      +LL+
Sbjct  1384  DSKTCEDIDECIDILGSCSQHCYNMRGSFRCSCTGYMLES DGRTCKV---TASESLLLLV  1440

Query  204    ANSQNILA-TYLSGAQVSTITPTSTRQTTAMDFSANETVCWVHVGD SAAQTQLKCARMP  262
          A+   I+A + S      +   A+DF  + + W      A Q + A
Sbjct  1441  ASQNKIIADSVTSQVHNIYSLVENGSIYIVAVDFDSISGRIFW----SDATQGKTWSAFQN  1496

Query  263    GLKGFVDEHTINISLSLHHVEQMAIDWLTGNFYFVDDIDDRIFVCNRNGDTCVTLLDLEL  322
          G      + +   S+   E +AIDW+ N Y+ D  + I V  +G      L+ L
Sbjct  1497  G-----TDRRVVFDSSIILTETIAIDWVGRNLYWTDYALETIEVSKIDGSHRTVLISKNL  1551

Query  323    YNPKGIALDPAMGK--VFFTDYGQIPKVERCDMDGQNRTKLVD SKIVFPHGITLDLVSRL  380
          NP+G+ALDP M +  +F++D+G P++ER MDG RT +V KI +P G+T+D +RL
Sbjct  1552  TNPRGLALDPRMNEHLLFWSDWGHHPRIERASMDGSMRTVIVQDKIFWPCGLTIDYPNRL  1611

Query  381    VYWADAYLDYIEVVDYEG-KGRQTIIQGILIEHLYGLTVFENYLYATNSDNANAQKTSV  439
          +Y+ D+YLDY++ DY G  RQ I  ++I H Y LT+FE+ +Y T D A  + V
Sbjct  1612  LYFMDSYLDYMDFCDYNGHHRRQVIASDLIIRHPYALTLFEDSVYWT--DRATRR----V  1665

Query  440    IRVNRFNSTEQVVT-RVDKGGALHIYHQRQPRVRSHACENDQYKPGGCS DICLLAN-  497
          +R N+++   VV  +      +   H +QP  + C  +      CS +CLL++
Sbjct  1666  MRANKWHGGNQSVVMYNIQWPLGIVAVHPSKQPN-SVNPCAFSR-----CSHLCLLSSQ  1718

Query  498    SHKARTCRCRSGFSLGSDGKSCCKPEHEFLVYGKGRPGIIRGMDMGAKV-PDEHMIPIE  556
          +C C SG+SL D  +C + +   +   R II G+ +  +V ++ M+PI
Sbjct  1719  GPHFYSCVCPSGWSLSPDLLNCLRDDQPFLITV---RQHIIFGISLNPEVKSNDAMVPIA  1775

Query  557    NLMNPRALDFHAETGFIYFADTTSYLIGRQKIDGTERETILKDGIHNVE-GVAVDWMGDN  615
          + N  ++F  +IY+ +   I R K DGT R      +   +A+DW+ N
Sbjct  1776  GIQNGLDVEFDDAEQYIYVVENPGE-IHRVKTDGTNRTVFASISMVGPSMNLA LDWISRN  1834

Query  616    LYWTDDGPKKTISVARLEKAAQTRKTLIEGKMT-----HPRAIVVDPLNGWMYWTDWEED  670
          LY T+   ++I V L  + RKTLI  T      P I VDP G +YW+D  D
Sbjct  1835  LYSTNP-RTQSIEVLTLHGDIRYRKTLIANDGTALGVGFPIGITVDPARGKLYWSDQGTD  1893
```

```
Query 671 PKDSRRGRLEAWMDG-SHRDIFVTSKTVLWPNGLSLDIPAGRLYWVDAFYDRIETILLN 729
      ++ A MDG S + +F + L ++LDI +LYW IE ++
Sbjct 1894 --SGVPAKIASANMDGTSVKTLFTGNLEHL--ECVTLDIEEQKLYWAVTGRGVIERGNVD 1949

Query 730 GTDRKIVYEGPELNHAFGLCHHGNYLFWTEYRSGSVYRLERGVGGAPPTVTLLRSEPPPI 789
      GTDR I+ +L+H +G+ H ++L++T+ + + R+++ G +LR P +
Sbjct 1950 GTDRMILVH--QLSHPWGIADVHDSFLYYTDEQYEVIERVDKATGA--NKIVLRDNVPNL 2004

Query 790 FEIRMYDAQQQQVGTNKRNVNNGCSSLCLATPGSR-QCACAEDQVLDADGVTCCLANPSY 848
      +++Y + +N C N C +CL PG CACA L+ D +C S+
Sbjct 2005 RGLQVYHRRNAAESSNGCSNNMNACQQICLPVPGGLFSCACATGFKLNPDNRSCSPYNSF 2064

Query 849 V 849
      +
Sbjct 2065 I 2065
```



Score = 320 bits (819), Expect = 4e-84

Identities = 219/745 (29%), Positives = 324/745 (43%), Gaps = 93/745 (12%)

```
Query 3453 CAPNQFQCSITKRCIPRVWVCDRDNDCVDGSDEPANCTQMTCGVDEFRCCKDSGRCIPARW 3512
      C F+C + CIP W CD DC D +DE C +TC F+C+ G+CIP W
Sbjct 28 CDSAHRFCG-SGHCI PADWRC DGT KDCSDDADE-IGCAVVT CQQGYFKCQSEGQCIPNSW 85

Query 3513 KCDGEDDCGDGSDEPKKECDERTCEPYQFRCKNNRCVPGRWQCDYDND CGDNSDEESCTP 3572
      +D D + +++C + TC +Q C N +C+P ++CD+ DC D +DE C
Sbjct 86 -VCDQDQDCDDGS DERQDCS QSTCSSHQITCSNGQCIPSEYRCDHVRDCPDGADENDCQY 144

Query 3573 RPCSESEFSCANGRCIAGRWKCDGDHDCADGSDEKDCTPRCDMDQFQCKSGHCIPLRWRC 3632
      C + +C NG C KCD DC D SDE +CT C ++F C +G CIP + C
Sbjct 145 PTCEQ--LTCDNGACYNTSQKCDWKVDCRDSSDEINCTEICLNHNEFSCGN GECIPRAYVC 202

Query 3633 DADADCMDGSDEEACGTGVRTCPLDEFQCNNTLCKPLAWKCDGEDDCGDNSDENPEECAR 3692
      D D DC DGSDE AC TC +F C + C W CDGEDDC DN DE+ E
Sbjct 203 DHDNDCQDGSDEHACN--YPTCGGYQFTCPSGRCIYQNWVCDGEDDCKDNGDEDGCESG- 259

Query 3693 FVCPNRPFRCKNDRVCLWIGRQCDGTDNCGDGTDEEDCEPPTAHTTHCKDKKEFLC-RN 3751
      H H +E+ C +
Sbjct 260 -----PHDVHKCSPREWSCPES 276

Query 3752 QRCLSSSLRCNMFDDCGDGSDEEDCSIDPKLTSCATNASICGDEARCVRTEKAAYCACRS 3811
      RC+S C+ DC DE + S + +A C + +C T C C
Sbjct 277 GRCISIIYKVC D GILDCP GRE DENNTSTGKYCSMTLCSALNC--QYQCHETPYGGACFCPP 334

Query 3812 GFHTVPGQPG-CQDINECLRFGTCSQLCNNTKGGHLCSCARNF-MKTHNTCKAEGSEYQV 3869
      G+ C + ++C +G C Q C + G HLC C + ++ CKA S +
Sbjct 335 GYIINHNSR TCVEFDDCQIWIGICDQKCESRPGRHLCHEEGYILERGQYCKANDSFGEA 394

Query 3870 LYIADDNEIRSLFP GHPHS-AYEQAFQGD ESVRIDAMDVHV KAGRVYWTNWHTGTISYRS 3928
      I + R L G H ++ + + H RV+WT+
Sbjct 395 SIIFSNG--RDLLIGDIHGRSFRILVESQNRGVAVGVAFHYHLQRVFWTD----- 442

Query 3929 LPPAAPPTTSNRHRRQIDRGVT---HLNISGLKMPRGIAIDWVAGNVYWTDSGRDVIEVA 3985
      T N+ G+ LN+S ++ P +A+DWV +Y ++ + I++
Sbjct 443 -----TVQNKVFSVDINGLNIQEVLNVS-VETPENLAVDWVNNKIYLVETKVN RIDMV 494

Query 3986 QMKGENRKT LISGMIDE PHAIVVDPLRG TMYWSDW---GNHPKIETAAMDGTLRET LVQD 4042
      + G R TLI+ + P I VDP G +++SDW PK+E A MDG+ R+ LV+
Sbjct 495 NLDGSYRVTLITENLGHPRGIAVDPTVGYLFFSDWESLSGEPKLERAFMDGSNRKD LVKT 554
```

Query 4043 NIQWPTGLAVDYHNERLYWADAKLSVIGSIRLNGTDPIVAADSKRGLSHPFPSIDVFEDI 4102
+ WP G+ +D ++R+YW D++ I ++ +G + HPF + +FE +
Sbjct 555 KLGWPAGVTLDMISKRVYVWDSRFDYIETVTYDGIQRKTVVHGGSLIPHPFGVSLFEGQV 614

Query 4103 YGVTYINNRFVKIHKFGH-SPLVNLTGGLSHASDVVLYHQHKQPEVTNPC--DRKKCEWL 4159
+ + V K +KF +P V L V +YH +QP TNPC + CE +
Sbjct 615 FFTDWTKMAVLKANKFTETNPQVYYQASL-RPYGVTVYHSLRQPYATNPCKDNNGGCEQV 673

Query 4160 CLLSPS-----GPVCTCPNGKRLD 4178
C+LS G C C G +LD
Sbjct 674 CVLSHRTDNDGLGFRCKCTFGFQLD 698



Score = 263 bits (671), Expect = 6e-67

Identities = 166/497 (33%), Positives = 253/497 (50%), Gaps = 40/497 (8%)

Query 25 KTCSPKQFACRDQITCISKGWRCDDGERDCPDGSDEAPEICPQSKAQRCQPNEHNCLGTEL 84
+TC QF C++ CISK + CD + DC DGSDE +C + C P+E C
Sbjct 3030 QTCQQNQFTCQNG-RCISKTFVCEDEDNDCGDSDELMLHC-HTPEPTCPPHEFKC-DNGR 3086

Query 85 CVPMSRLCNGVQDCMDGSDE-GPHCRELQGNCSRLGCQHHCVPPTLDGPTCYCNSSFQLQA 143
C+ M +LCN + DC+D SDE G E + S GC H+C TL C C ++L +
Sbjct 3087 CIEMMKLCNHLDDCLDNSDEKGCGINECH-DPSISGCDHNCTDTLTSFYCSCRPGYKLMS 3145

Query 144 DGKTCKDFDECSVYG-TCSQLCTNTDGSFICGVEGYLLQPDNRSCAKNEPVDRPPVLL 202
D +TC D DEC+ CSQ C N GS+IC C GYL +PD ++C+ +N ++ P L+
Sbjct 3146 DKRTCDVIDECTEMPFVCSQKCENVIGSYICKCAPGYLREPDGKTCR-QNSNIE--PYLI 3202

Query 203 IANSQNILATYLSGAQVSTITPTSTRQTTAMDFSANETVCWVHVGDSAAQTQLKCAMP 262
+N + + G S I A+DF + + W+ TQ +
Sbjct 3203 FSNRYYLRLNLTIDGYFYSLILEGLDNVV-ALDFDRVEKRLYWI-----DTQRQVIERM 3254

Query 263 GLKGFVDEHTINISLSLHHVEQMAIDWLTGNFYFVDDIDDRIFVCNRNG-----DTCV 315
L E IN L E +A+DW++ Y++D D +FV + NG CV
Sbjct 3255 FLNKTNKETIINHRLPA--AESLAVDWVSRKLYWLDARLDGLFVSDLNGGHRMLAQHCV 3312

Query 316 TLLDLELY-NPKGIALDPAMGKVFFTDYQGIPKVERCDMDGQNRKLVDSKIVFPHGITL 374
+ + NP+G+AL P G +++ D+G + R MDG N++ ++ +K+ +P+GIT+
Sbjct 3313 DANNTFCFDNPRGLALHPQYGYLYWADWGHRAIYGRVGMGTNKSIIISTKLEWPNGITI 3372

Query 375 DLVSRLVYWADAYLDYIEVVDYEGKGRQTIIQILIEHLYGLTVFENYLYATNSDNANAQ 434
D + L+YWADA+L YIE D EG R T+ G L H + +T+FE+ +Y T+ +
Sbjct 3373 DYTNDLLYWADAHLGYIEYSDLEGHHRHTVYDGL-PPFAITIFEDTIYWDWNT---- 3427

Query 435 QKTSVIRVNRFNSTEQ-VVTRVDKGGALHIYHQRQPRVRSHACENDQYGKPGGCSDIC 493
+V + N+++ + Q +V + +H+YH RQP V + N+ GGCS +C
Sbjct 3428 --RTVEKGNKYDGSNRQTLVNTTHRPFDIHVYHPYRQPIVSNPCGTNN----GGCSHLC 3480

Query 494 LLANSHKARTCRCSGF 510
L+ K TC C F
Sbjct 3481 LIKPGGKGFTCECPDDF 3497



Score = 220 bits (561), Expect = 3e-54

Identities = 113/286 (39%), Positives = 148/286 (51%), Gaps = 12/286 (4%)

Query 3413 CLPSQFKCTNTNRCIPGIFRCNGQDNCGDGEDERDCPEVTCAPNQFQCSITKRCIPRVWV 3472
C + F+C + CIP +RC+G +C D DE C VTC F+C +CIP WV
Sbjct 28 CDSAHFRC-GSGHCIPADWRCDGDKDCSDDADEIGCAVVTCQQGYFKCQSEGQCIPNSWV 86

Query 3473 CDRDNCVDGSDSEPANCTQMTGCVDEFRCCKDSGRCIPARWKCDGEDDCGDGSDEPKEECD 3532
CD+D DC DGSDE +C+Q TC + C +G+CIP+ ++ + +C
Sbjct 87 CDQDQDCDDGSDERQDCSQSTCSSHQITC-SNGQCIPSEYR--CDHVRDCPDGADENDCQ 143

Query 3533 ERTCEPYQFRCKNNRCVPGRWQCDYDNCGDNSDEESCTPRPCSESEFSCANGRCIAGRW 3592
TCE Q C N C +CD+ DC D+SDE +CT C +EFSC NG CI +
Sbjct 144 YPTCE--QLTCDNGACYNTSQKCDWKVDCRDSSDEINCT-EICLHNEFSCGNCECIPRAY 200

Query 3593 KCDGDHDCADGSDEKDCT-PRCDMDQFQCKSGHCIPLRWRCADADCMDGSDEEACGTG- 3650
CD D+DC DGSDE C P C QF C SG CI W CD + DC D DE+ C +G
Sbjct 201 VCDHDNDQCQDGSDEHACNYPTCGGYQFTCPSGRCIYQNWVCDGEDDCKDNGDEDGCESGP 260

Query 3651 --VRTCPLDEFQC-NNTLCKPLAWKCDGEDDCGDNSDENPEECARF 3693
V C E+ C + C + CDG DC DEN ++
Sbjct 261 HDVHKCSPREWSCPESGRCSISYKVC DGILDCPGREDENNTSTGKY 306



Score = 209 bits (532), Expect = 8e-51

Identities = 123/350 (35%), Positives = 166/350 (47%), Gaps = 41/350 (11%)

Query 3373 KCRPGQFQCSTGICTNPAFICDGDNDQCQDNSDEANCDIHVCLPSQFKCTNTNRCIPGIFR 3432
+C F+C +G C + CDG DC D++DE C + C FKC + +CIP +
Sbjct 27 ECDSAHFRCGSGHCIPADWRCDGDKDCSDDADEIGCAVVTCQQGYFKCQSEGQCIPNSWV 86

Query 3433 CNGQDNCGDGEDER-DCPEVTCAPNQFQCSITKRCIPRVWVCDRDNCVDGSDSEPANCTQ 3491
C+ +C DG DER DC + TC+ +Q CS +CIP + CD DC DG+DE +C
Sbjct 87 CDQDQDCDDGSDERQDCSQSTCSSHQITCS-NGQCIPSEYRCDHVRDCPDGADE-NDCQY 144

Query 3492 MTCGCVDEFRCCKDSGRCIPARWKCDGEDDCGDGSDEPKEECDERTCEPY----QFRCKNNR 3547
TC ++ C D+G C KCD + DC ++ DE C +F C N
Sbjct 145 PTC--EQLTC-DNGACYNTSQKCDWKVDC-----RDSSDEINCTEICLHNEFSCGNGE 194

Query 3548 CVPGRWQCDYDNCGDNSDEESCTPRPCSESEFSCANGRCIAGRWKCDGDHDCADGSDEK 3607
C+P + CD+DNDC D SDE +C C +F+C +GRCI W CDG+ DC D DE
Sbjct 195 CIPRAYVCDHDNDQCQDGSDEHACNYPTCGGYQFTCPSGRCIYQNWVCDGEDDCKDNGDED 254

Query 3608 DC-----TPRCMDQFQC-KSGHCIPLRWRCADADCMDGSDEEACGTGVRTCPLDEFQ 3660
C +C ++ C +SG CI + CD DC DE TG
Sbjct 255 GCESGPHDVHKCSPREWSCPESGRCSISYKVC DGILDCPGREDENNTSTGK-----Y 306

Query 3661 CNNTLCKPLAWKCDGEDDCGDNSDENPEECARFVCPNRPFRCKNDRVCL 3710
C+ TLC L +C E P A F CPP + R C+
Sbjct 307 CSMTLCSAL-----NCQYQCHETPYGGACF-CPPGYIINHNSRTECV 347



Score = 174 bits (440), Expect = 4e-40

Identities = 107/302 (35%), Positives = 135/302 (44%), Gaps = 55/302 (18%)

```

Query 3331 VSNCTASQFVCKND-KCIPFWWKCDTEDDCGDHSDEPPDCPEFKCRPGQFQCSTGICTNP 3389
          V  C    F C+++ +CIP W CD + DC D SDE DC + C  Q  CS G C
Sbjct 64   VVTCQQGYFKCQSEGQCIPNSWVCDQDQDCDDGSDERQDCSQSTCSSHQITCSNGQCIPS 123

Query 3390 AFICDGDNDQCQDNSDEANCDIHVCLPSQFKCTNTNRCIPGIFRCNGQDNCGDGEDERDCP 3449
          + CD  DC D +DE +C  C  Q  C N  C    +C+ + +C D  DE +C
Sbjct 124  EYRCDHVRDCPDGADENDCQYPTC--EQLTCDN-GACYNTSQKCDWKVDCRDSSDEINCT 180

Query 3450 EVTCAPNQFQCSITKRCIPRVWVCDRDNDQDGSDEPANCTQMTTCGVDEFRCCKDSGRCIP 3509
          E+ C  N+F C    CIPR +VCD DNDC DGSDE A C  TCG +F C  SGRCI
Sbjct 181  EI-CLHNEFSCG-NGECIPRAYVCDHDNDQDGSDEHA-CNYPTCGGYQFTC-PSGRCI- 235

Query 3510 ARWKCDGEDDCGDGSDEPKKEECDERTCEPYQFRCKNNRCVPGRWQCDYDNDQDNDSDDEES 3569
          YQ                                W CD ++DC DN DE+
Sbjct 236  -----YQ-----NWVCDGEDDCKDNGDEEDG 255

Query 3570 CTPRP-----CSESEFSC-ANGRCIAGRWKCDGDHDCADGSDEKDCPTRCDMDQFQCKSG 3623
          C  P    CS  E+SC  +GRCI+  CDG DC  DE + +  C +
Sbjct 256  CESGPHDVHKCSPREWSCPESGRCISIIYKVC DGILDCPGREDENNTSTGKYCSMTLCSAL 315

Query 3624 HC 3625
          +C
Sbjct 316  NC 317

```



Score = 159 bits (402), Expect = 1e-35

Identities = 165/632 (26%), Positives = 240/632 (37%), Gaps = 109/632 (17%)

```

Query 3817 PGQPGCQDINECLRF-GTCSQLCNNTKGGHL--CSCARNFMKTHNTCKAEGSEYQVLYIA 3873
          P  P  + N CL  G CS LC  G H  C CA  +++  A +E  L  A
Sbjct 2335 PRSPAENVNNPCLENNGGCSHLCLFALPGLHTPKCDCAFGLTQSDGKNCAISTE-NFLIFA 2393

Query 3874 DDNEIRSL-FPGHPHSAYEQAFQGDSEVRIDAMDVHVKAGRVYWTN--WHTGTISYRSL 3929
          N +RSL  HS  Q  + +V  ++D  + R+Y+T  G ISY +L
Sbjct 2394 LNSLSRLSLHLDPENHSPPFQTINVERTVM--SLDYDSVSDRIYFTQNLASGVGQISYATL 2451

Query 3930 PPAAPPTTSNRHRRQIDRGVTHLNISGLKMPRGIAIDWVAGNVYWTDSGRDVIEVAQMKG 3989
          T  + SG+  GIA DW+  +Y++D  +I  G
Sbjct 2452 SSGIHTPT-----VIASGIGTADGIAFDWITRRIYSDYLNQMINSMAEDG 2497

Query 3990 ENRKT LISGMIDEPHAIVVDPLRGTMYSWDGWNHPKIEAAMDGTLRETLVQDNIQWPTG 4049
          NR  +  + +P AIV+DP +G +YW+DW  H KIE A + G  R  +V  ++  P+G
Sbjct 2498 SNRTVI--ARVPKPRAIVLDPCQGYLYWADWDTHAKIERATLGGNFRVPIVNSSLVMPSPG 2555

Query 4050 LAVDYHNERLYWADAKLSVIGSIRLNGTDPIVAADSKRGLSHPFSDVFEYIYGVTYIN 4109
          L +DY  + LYW DA L  I  L G D V  ++  H F + ++  YIY
Sbjct 2556 LTLDYEEDLLYWVDASLQRIERSTLTGVDREVIVNA---AVHAFGLTLYGQYIYWTDLYT 2612

Query 4110 NRVFKIHKF-GHSPLVNLTGGLSHASDVVLYHQHKQPEVTNPCCRKK--CEWLCLLSPSG 4166
          R+++ +K+ G S  + T LS  +  ++++ + NPC++  C +C  P+G
Sbjct 2613 QRIYRANKYDGSQIAMTTNLLSQPRGINTVVKNQKQQCNPCEQFNGGCSHCAPGPNG 2672

Query 4167 PVCTCPNGKRLDNGTCVPVPSPTPPPDAPRPGTCNLQCFNGGSCFLNARRQPKCRCQPRY 4226
          C CP+  N  + R G  + C NG  RC
Sbjct 2673 AECQCPHE---GNWYLANNRKHCIVDNGERCASSFTCSNG-----RCISEE 2716

Query 4227 TGDKCELDQCWEHCRNGGTCAASPSGMPTCRCPTGFTGPKCTQQVCAGY---CANNSTC- 4282
          KC+ D  C +G  S  + TC  PT FT  C  C  Y  C  + C

```

Sbjct 2717 W--KCDND---NDCGDSDEMESVICALHTC-SPTAFT---CANGRCVQYSYRCDYND CG 2767

Query 4283 -----TVNQGNQPQC---RCLP-GFLGD-----RCQYRQC-SGY- 4311
N + C RC+P F+ + C R C SGY

Sbjct 2768 DGSDEAGCLFRDCNATTEFCMNNRRCIPREFICNGVDNCHDNNTSDEKNCPCDRTCQSGYT 2827

Query 4312 -CENFGTC---QMAADGSRQCRCTAYFEGSRCEVNKCS---RCLEGACVVNKQSGDVTC 4363
C N C DG C + + C + CS +C G C+ D

Sbjct 2828 KCHNSNICIPRVYLCGDGNDNCGDNSDENPTYCTTHTCSSEFQCASGRCIPQHWYCDQET 2887

Query 4364 NCTDGRVAP-----SCLTCVGHCSNGGSC 4387
+C D P +CL C +GG C

Sbjct 2888 DCFDASDEPASCGHSERTCLADEFKC-DGGRC 2918



Score = 153 bits (387), Expect = 5e-34

Identities = 89/244 (36%), Positives = 119/244 (48%), Gaps = 28/244 (11%)

Query 2513 DDLTCRAVNSSCRAQDEFEC-ANGECINFSLTCDGVPHCKDKSDEKPSYCNSRRCKKTFR 2571
D++ C V +C+ Q F+C + G+CI S CD C D SDE+ C+ C

Sbjct 58 DEIGCAVV--TCQ-QGYFKCQSEGQCIPNSWVCDQDQDCDDGSDERQD-CSQSTCSSHQI 113

Query 2572 QCSNGRCVSNMLWCNGADDCGDSDEIPCNKTACGVGEFRCDGTICIGNSSRCNQFVDCE 2631
CSNG+C+ + C+ DC DG+DE C C + C +G C S +C+ VDC

Sbjct 114 TCSNGQCIPSEYRCDHVRDCPDGADENDCQYPTCE--QLTCDNGACYNTSQKCDWKVDCR 171

Query 2632 DASDEMNC SATDCSSYFRLGVKGVLFPQCERTSLCYAPSWVCDGANDCGDYSDERDCPGV 2691
D+SDE+NC+ + F G C ++VCD NDC D SDE C

Sbjct 172 DSSDEINCTEICLHNEFSCG-----NGECIPRAYVCDHDNDCQDGSDEHAC--- 217

Query 2692 KRPRCPLNYFACPSGRCIPMSWTCDKEDDCEHGEDETHCNK-----FCSEAQFEC-QNH 2744
P C F CPSGRCI +W CD EDDC+ DE C CS ++ C ++

Sbjct 218 NYPTCGGYQFTCPSGRCIYQNWVCDGEDDCKDNGDEDCESGPHDVHKCSPREWSCPESG 277

Query 2745 RCIS 2748
RCIS

Sbjct 278 RCIS 281



Score = 122 bits (305), Expect = 2e-24

Identities = 99/276 (35%), Positives = 128/276 (46%), Gaps = 29/276 (10%)

Query 801 QVGTNKRVRNNGGCSSLCLATPGSRQACAEDQVLADGVTCLANPSYVPPPQCQPGEFA 860
Q G KC+ + G C + C D+ D TC ++ QC P E+

Sbjct 68 QQGYFKCQ-SEGQCIPNSWVCDQDQDCDDGSDERQDCSQSTCSSHQITCSNGQCIPSEY- 125

Query 861 CANSRCIQERWKCDGNDCLDNSDEAPALCHQHTCPSDRFKCENNRCIPNRWLCGDNDNC 920
+CD DC D +DE C TC ++ C+N C CD DC

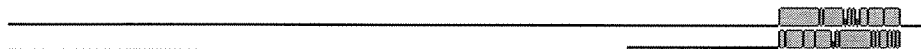
Sbjct 126 -----RCDHVRDCPDGADEND--CQYPTC--EQLTCDNGACYNTSQKCDWKVDC 170

Query 921 GNSEDES NATCSARTCPPNQFSCASGRCIPISWTCDLDDDCGDRSDESASCAYPTCFPLT 980
+S DE N T C N+FSC +G CIP ++ CD D+DC D SDE A C YPTC

Sbjct 171 RDSSDEINCT---EICLHNEFSCGNCECIPRAYVCDHDNDCQDGSDEHA-CNYPTCGGY- 225

Query 981 QFTCNNGRCININWRCNDNDNDCGDNDSDEAGCS-----HSCSSTQFKC-NSGRCIPEHWT 1033
QFTC +GRCI NW CD ++DC DN DE GC H CS ++ C SGRCI +
Sbjct 226 QFTCPSGRCIYQNWVCDGEDDCKDNGDEDGCESGPHDVHKCSPREWSCPESGRCISIIYKV 285

Query 1034 CDGDNDGCDYSDETHANCTNQATRPPGGCHTDEFQC 1069
CDG DC DE + + + ++QC
Sbjct 286 CDGILDCPGREDENNTSTGKYCSMTLCSALNCQYQC 321



Score = 119 bits (298), Expect = 1e-23

Identities = 117/488 (23%), Positives = 191/488 (39%), Gaps = 66/488 (13%)

Query 3963 IAIDWVAGNVYWTDSGRDVIEVAQMKGENRKTLSGMIDEPHAIVVDPLRGTMYSWDWGN 4022
+A DW++ N+YWTDS I V ++ + R+T++ ++ P ++VV P G ++++DW
Sbjct 789 LAFDWISKNLTYWTDSHYKSISVMRLADKTRRTVVQ-YLNNPRSVVHPFAGYLFSTDWFR 847

Query 4023 HPKIETAAMDGTLRETLVQDNIQWPTGLAVDYHNERLYWADAKLSVIGSIRLNGTDPIVA 4082
KI A DG+ ++ + WP GLA+D+ RLYW DA I +G D
Sbjct 848 PAKIMRAWSDGSHLLPVINTTLGWPNGLAIDWAASRLYWVDAYFDKIEHSTFDGLDRRL 907

Query 4083 ADSKRGLSHPFSDIDVFEDIYGVTYINNRVFKIHKFGHSPLVNLTGGLSHASDVVLYHQH 4142
++ ++HPF + +F ++++ + + ++ K + + G+++ + Y +
Sbjct 908 GHIEQ-MTHPFGLAIFGEHLFFTDWRLGAIIRVRKADGGEMTVIRSGIAYILHLKSYDVN 966

Query 4143 KQPEVTNPICDRK-----KCEWLCLLSPS-GPVCTCPNGKRLDNGTCVPVPSPTPPPDAPR 4196
Q +N C++ C C P+ VC CP G RL + PT P +
Sbjct 967 IQTG-SNACNQPTHPNGDCSHFCFPVPNFQRVCGCPYGMRLASNHLTCEGDPTNEPPTAQ 1025

Query 4197 PGTCNLQCFNGGSCFLNARRQPKCRCQPRYTGDKE-LDQCWEHCRN-----GGTCAAS 4249
G + C NG RC P Y C+ +D C ++ TC++S
Sbjct 1026 CGLFSFPCKNG-----RCVPNY--LCDGVDDCHDNSDEQLCGTLNNTCSSS 1070

Query 4250 --PSGMPTC-----RCPTGFTGPKCTQQVCAGYCANNSTCTVNQGNQPCRC-L 4295
G C C G C A TC +Q C
Sbjct 1071 AFTCGHGECIPAHWRCDKRNDCVDGSDEHNCPTHAPASCLDTQYTCDNHQCISKNWVCDT 1130

Query 4296 PGFLGDRCQYRQCSGYCENFGTCQMAADGSRQCRCTAYFEGSRCEVNKCSRCLEGA---- 4351
GD + C+ + TCQ + RC C+ +K C++G+
Sbjct 1131 DNDGCGDSDEKNCN---STETCQPSQFNCPNHRICIDL--SFVCDGDK--DCVDGSDEVG 1182

Query 4352 CVVKNQSGDVTNCTDGRVAPSCLTCVGHCSNGGSCTMNSKMMPECQCPHMTGPRCEEH 4411
CV+N + C D C+ C C+ NS E CP G C
Sbjct 1183 CVLNCTASQFKCASGD-----KCIGVTNRCDGVFDCSDNS---DEAGCPTRPPG-MCHSD 1233

Query 4412 VFSQQQPG 4419
F Q+ G
Sbjct 1234 EFQCQEDG 1241



Score = 104 bits (259), Expect = 4e-19

Identities = 61/180 (33%), Positives = 84/180 (46%), Gaps = 21/180 (11%)

Query 3297 NNGGCSNLCLLSPGGGHKACPTNFYLGSDGRTCVSNCTASQFVCKNDKCIPFWWKCDTE 3356
+NG C N KC + SD C C ++F C N +CIP + CD +

Sbjct 153 DNGACYNT-----SQKCDWKVDCRDSSDEINCTEICLHNEFSCGNGECIPRAYVCDHD 205

Query 3357 DDCGDHSDEPPDCPEFKCRPGQFQCSTGICTNPAFICDGDNDQCQNSDEANC-----DIH 3411
+DC D SDE C C QF C +G C ++CDG++DC+DN DE C D+H

Sbjct 206 NDCQDGSDEHA-CNYPTCGGYQFTCPSGRCIYQNWVCDGEDDCKDNGDEDGCESGPHDVH 264

Query 3412 VCLPSQFKCTNTNRCIPGIFRCNGQDNCGDGEDERD-----CPEVTCAP--NQFQCSIT 3463
C P ++ C + RCI C+G +C EDE + C C+ Q+QC T

Sbjct 265 KCSPREWSCPESGRCISIIYKVCDGILDCPGREDENNTSTGKYCSMTLCSALNCQYQCHET 324



Score = 94.0 bits (232), Expect = 5e-16

Identities = 75/261 (28%), Positives = 98/261 (37%), Gaps = 36/261 (13%)

Query 2490 QDLCLLTHQGHVNCSCRGGRILQDDLTCRAVNSSCRAQDEFECA-----NGECIN 2539
QD T H +C G+ + + C V DE +C NG C N

Sbjct 101 QDCSQSTCSSH-QITCSNGQCIPSEYRCDHVRDCPDGADENDCQYPTCEQLTCDNGACYN 159

Query 2540 FSLTCDGVPHCKDKSDEKPSYCNSRRCKKTFRQCSNGRCVSNMLWCNGADDCGDGSDEIP 2599
S CD C+D SDE + C C NG C+ C+ +DC DGSDE

Sbjct 160 TSQKCDWKVDCRDSSDEINC--TEICLHNEFSCGNGECIPRAYVCDHDNDQCQDGSDEHA 216

Query 2600 CNKTACGVGEFRCDGTICIGNSSRCNQFVDCEDASDEMNC SATDCSSYFRLGVKGVLFQP 2659
CN CG +F C G CI + C+ DC+D DE C S +

Sbjct 217 CNYPTCGGYQFTCPSGRCIYQNWVCDGEDDCKDNGDEDGCE----SGPHDVHKCSPREWS 272

Query 2660 CERTSLCYAPSWVCDGANDCGDYSDERDCPGVK-----RPRCPLNYFA----C 2703
C + C + VCDG DC DE + K + +C + C

Sbjct 273 CPESGRCISIIYKVCDGILDCPGREDENNTSTGKYCSMTLCSALNCQYQCHETPYGGACFC 332

Query 2704 PSGRCIPM--SWTCDKEDDCE 2722
P G I S TC + DDC+

Sbjct 333 PPGYIINHNDSTRCTVEFDDCQ 353



Score = 78.6 bits (192), Expect = 2e-11

Identities = 46/109 (42%), Positives = 57/109 (52%), Gaps = 10/109 (9%)

Query 23 APKTCSPKQFACRDQITCISKGWRCGERDCPDGSDEAPEICPQSKAQRCQP-NEHNCLG 81
A +TC P QF C + CI + W+CD + DC D SDE E C S A C E +C

Sbjct 3631 ASRTCPRGQFRCANG-RCIPQAWKCDVDNDCGDHSDEPIEEC-MSSAHLCDNFTEFSCKT 3688

Query 82 TELCVPM SRLCNGVQDCMDGSDEGPHCRELQGNCSRLG---CQ-HHCVP 126
C+P +CNGV DC D SDE C E C +G C+ HHC+P

Sbjct 3689 NYRCIPKWAVCNGVDDCRDNDSE-QGCEE--RTCHPVGDFRCKNHHCIP 3734



Score = 78.2 bits (191), Expect = 3e-11

Identities = 93/430 (21%), Positives = 162/430 (37%), Gaps = 72/430 (16%)

Query 25 KTCSPKQFACRDQITCISKGWRCDCGERDCPDGSDEAPEICPQSKAQRCQPNEHNCLGTE- 83
+TC +F C D CI W CDG+ DC D SDE Q + Q C +E C+
Sbjct 2904 RTCLADEFKC-DGGRCIPSEWICDGDNDGDMSEDEK--HQCQNQNCSDSEFLCVNDRP 2960

Query 84 ---LCVPMSRLCNGVQDCMDGSDEGPHCRELQGNCSRLGQCQHH-CVPTLDGPTCYCNSSF 139
C+P S +C+G DC DG DE +C + + C + C+P + C ++
Sbjct 2961 PDRRCIPQSWVCDGDVDCDGYDENQNCNTRTCSENEFTCGYGLCIPKIF--RCDRHND 3018

Query 140 QLQADGKTCKDFDECSVYGTCQ---LCTN---TDGSFIC----GCVEG-----YLLQPD 184
+D + C +Y TC Q C N +F+C C +G +L
Sbjct 3019 GDYSDEGRC-----LYQTCQQNQFTCQNGRCISKTFVCEDEDNDCGDSDELMHLCHTP 3071

Query 185 NRSCAKNEPVDPRPPVLLIANSONILATYLSGAQVSTITPTSTRQTTAMDFSANETVCW 244
+C D + + N L L + + ++
Sbjct 3072 EPTCPPHEFKCDNGRCIEMMKLCNHLDDCLDNSDEKGCINECH-----DPSISG 3121

Query 245 VHVGDAAQTQLKCARMPGLKGFVDEHT---INISLSLHHVEQMAIDWLTGNFY----- 295
+ T C+ PG K D+ T I+ + V + + G++
Sbjct 3122 CDHNCTDTLTSFYCSCRPGYKLMDSKRTCDVIDECTEMPFVCSQKCEENVIGSYICKCAPG 3181

Query 296 FVDDIDDRIFVCNRNGDTCVTLLEDLYNPKGIALD-----PAMGKVFFTDYGQIPK 347
++ + D + C +N + L+ Y + + +D + V D+ ++ K
Sbjct 3182 YLREPDGK--TCRQNSNIEPYLIFSNRYLRLNLTIDGYFYSLEGLDNVVALDFDRVEK 3239

Query 348 -----VERCDMDGQNRKLVDSKIVFPHGITLDLVSRVLVYWADAYLDYIEVVDY 396
+ER ++ N+ +++ ++ + +D VSR +YW DA LD + V D
Sbjct 3240 RLYWIDTQRQVIERMFLNKTNETI INHRLPAAESLAVDWVSRKLYWLDARLDGLFVSDL 3299

Query 397 EGKGRQTIIQ 406
G R+ + Q
Sbjct 3300 NGGHRRLAQ 3309



Score = 73.2 bits (178), Expect = 9e-10

Identities = 44/139 (31%), Positives = 63/139 (45%), Gaps = 26/139 (18%)

Query 22 DAPKTCSPKQFACRDQITCISKGWRCDCGERDCPDGSDEAPEICPQSKAQRCQPNEHNCLG 81
++ +TC P QF C + CI + CDG++DC DGSDE + C ++ C
Sbjct 1144 NSTETCQPSQFNCNPH-RCIDLFSVCDGDKDCVDGSDEVGCVL-----NCTASQFKCAS 1196

Query 82 TELCVPMMSRLCNGVQDCMDGSDEGPHCRELQGNCSRLGQCQHHCVPTLDGPTCYCNSSFQL 141
+ C+ ++ C+GV DC D SDE GC PT C+ + FQ
Sbjct 1197 GDKCIGVTNRCDGVFDCSDNSDEA-----GC-----PTRPPGMCH-SDEFQC 1237

Query 142 QADGKTCKDFDECSVYGTC 160
Q DG +F EC + C
Sbjct 1238 QEDGICIPNFWECGHPDC 1256



Score = 72.8 bits (177), Expect = 1e-09

Identities = 54/170 (31%), Positives = 77/170 (45%), Gaps = 39/170 (22%)

Query 26 TCSPPKQFACRDQITCISKGWRCDCGERDCPDGSDEAPEICPQSKAQRCQPNEHNCLGTELC 85

```

Sbjct 66 TC F C+ + CI W CD ++DC DGSDE + C QS C ++ C + C
TCQQGYFKCQSEGQCIPNSWVCDQDQDCDDGSDERQD-CSQS---TCSSHQITCSNGQ-C 120

Query 86 VPMSRLCNGVQDCMDGSDEG----PHCRELQGNC SRLGCQHHCVP TLDGPTCYCNSSFQ L 141
+P C+ V+DC DG+DE P C +L T D CY S
Sbjct 121 IPSEYRCDHVRDCPDGADENDCQYPTCEQL-----TCDNGACYNTSQ--- 162

Query 142 QADGKT-CKD-FDECSVYGTC SQLCTNTDGSFICG---CV-EGYLLQPDN 185
+ D K C+D DE + C+++C + + F CG C+ Y+ DN
Sbjct 163 KCDWKVDCRDSSDEIN----CTEICLHNE--FSCGN GECIPRAYVCDHDN 206

```



Score = 69.7 bits (169), Expect = 1e-08

Identities = 52/165 (31%), Positives = 69/165 (41%), Gaps = 20/165 (12%)

```

Query 21 IDAPKTCSPKQFACRDQITCISKGWRC DGERDCPDGSDEAPEICPQSKAQRCQPNEHNCL 80
+D + C F C + CIS+ W+CD + DC DGSDE +C C P C
Sbjct 2694 VDNGERCGASSFTCSNG-RCISEEWKCDNDNDCGDGSDMESVC---ALHTCSPTAFTCA 2749

Query 81 GTELCVPM SRLCNGVQDCMDGSDE-GPHCRELQGNC SRLGCQHHCVP---TLDG-PTCYC 135
CV S C+ DC DGSDE G R+ + C+P +G C+
Sbjct 2750 NGR-CVQYSYRCDYYNDCGDGSD EAGCLFRDCNATTEFMCNNRRCIPREFICNGVDNCHD 2808

Query 136 NSSFQLQADGKTCKDFDECSVYGTC--SQLCTN----TDGSFICG 174
N++ +D K C D S Y C S +C DG CG
Sbjct 2809 NNT---SDEKNCPDRTCQSGYTKCHNSNICIPRVYLCGDND CG 2849

```



Score = 64.7 bits (156), Expect = 3e-07

Identities = 44/149 (29%), Positives = 60/149 (40%), Gaps = 13/149 (8%)

```

Query 25 KTCSPKQFACRDQITCISKGWRC DGERDCPDGSDEAPEICPQSKAQRCQPNEHNCLGT EL 84
+TC C + CI + + CDG+ DC D SDE P C C +E C +
Sbjct 2820 RTCQSGYTKCHNSNICIPRVYLCGDND CGD NSDENPTYC---TTHTCSSEFQC-ASGR 2875

Query 85 CVPMSRLCNGVQDCMDGSDEGPHCRELQGNC SRLGCQHHCVP TLDGPTCYCNSSFQ LQAD 144
C+P C+ DC D SDE C + C L + C DG C S + D
Sbjct 2876 CIPQHWYCDQETDCFDASDEPASC GHSERTC--LADEFKC---DGGRC-IPSEWICDGD 2928

Query 145 GKTCKDFDECSVYGTC SQLCTNTDGSFIC 173
DE + +Q C +D F+C
Sbjct 2929 NDCGDM SDEDKRHQCNQNC--SDSEFLC 2955

```



Score = 60.8 bits (146), Expect = 5e-06

Identities = 36/113 (31%), Positives = 47/113 (41%), Gaps = 20/113 (17%)

```

Query 23 APKTCSPKQFACRDQITCISKGWRC DGERDCPDGSDEAPEICPQSKAQRCQPNEHNCLGT 82
AP+ C+ +F C +Q CI W CD DC D SDE + + C P C

```

Sbjct 3755 APRECTESEFRCVNQ-QCIPSRWICDHYNDCGDNNDER-----DCEMRTCHPEYFQCTSG 3808

Query 83 ELCVPMSRLCNGVQDCMDGSDE-----GPHCRELQGNCSRLGCQHHCV 126
CV C+G DC+D SDE G +C+ C H C+P

Sbjct 3809 H-CVHSELKCDGSADCLDASDEADCPTRFPDGAYCQATMFECK----NHVCIP 3856



Score = 57.8 bits (138), Expect = 4e-05
Identities = 31/81 (38%), Positives = 43/81 (53%), Gaps = 8/81 (9%)

Query 25 KTCSPK-QFACRDQITCISKGWRCDCPDGSDEAPEICPQSKAQRCQPNEHNCLGTE 83
+TC P F C++ CI W+CDG+ DC D SDE E C + C +E C+ +

Sbjct 3717 RTCHPVGD FRCKNH-HCIPLRWQCDGQND CGDN SDE--ENC---APRECTESEFRCVNQQ 3770

Query 84 LCVPM SRLCNGVQDCMDGSDE 104
C+P +C+ DC D SDE

Sbjct 3771 -CIPSRWICDHYNDCGDN SDE 3790

CPU time: 0.08 user secs. 0.05 sys. secs 0.13 total secs.